

1154-57-1905 **Harrison Chapman*** (hchaps@gmail.com) and **Andrew Rechnitzer**. *A Markov chain sampler for knot diagrams.*

Knot diagrams provide a model for entanglement in physical polymers whose complexity is precisely the number of crossing regions where the polymer comes close to itself. As a DNA model, these crossing regions may be viewed as sites for the strand-passage action of type II topoisomerases.

Diagrams of fixed type become exponentially rare, and so efficient random generation is a difficult problem. We describe a new Markov chain Monte Carlo sampler for knot diagrams representing any fixed knot type, whose transitions are natural diagram moves. We prove that the limiting distribution of this Markov chain is the uniform distribution. Using this sampler, we examine a number of classical polymer statistics in the knot diagram model. We then explore topoisomerase unknotting pathways for circular DNA in the diagram model. (Received September 16, 2019)